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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/662,783

DATE: 09/26/2000
TIME: 11:55:50

Input Set : A:\Cura-77.app
Output Set: N:\CRF3\09262000\I662783.raw

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3 <110> APPLICANT: Lichenstein, Henri
4 Shimkets, Richard A.
5 Herrmann, John
6 Boldog, Ferenc
8 <120> TITLE OF INVENTION: Growth Factor Polypeptides and Nucleic Acids Encoding
9 Same
11 <130> FILE REFERENCE: 15966-577 (Cura-77)
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/662,783
14 <141> CURRENT FILING DATE: 2000-09-12
16 <150> PRIOR APPLICATION NUMBER: USSN 60/158,083
17 <151> PRIOR FILING DATE: 1999-10-07
19 <150> PRIOR APPLICATION NUMBER: USSN 60/186,707
20 <151> PRIOR FILING DATE: 2000-03-03
22 <150> PRIOR APPLICATION NUMBER: USSN 60/188,250
23 <151> PRIOR FILING DATE: 2000-03-10
25 <150> PRIOR APPLICATION NUMBER: USSN 60/159,231
26 <151> PRIOR FILING DATE: 1999-10-13
28 <150> PRIOR APPLICATION NUMBER: USSN 60/174,485
29 <151> PRIOR FILING DATE: 2000-01-04
31 <150> PRIOR APPLICATION NUMBER: USSN 60/223,879
32 <151> PRIOR FILING DATE: 2000-08-08
34 <160> NUMBER OF SEQ ID NOS: 24
36 <170> SOFTWARE: PatentIn Ver. 2.0
38 <210> SEQ ID NO: 1
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40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
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45 <222> LOCATION: (182)..(1291)
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52 gtcccgggag cagaaccggg ctttttcttg gagcgacgct gtctctagtc gctgatccca 180
54 a atg cac cgg ctc atc ttt gtc tac act cta atc tgc gca aac ttt tgc 229
55 Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
56 1 5 10 15
58 agc tgt cgg gac act tct gca acc ccg cag agc gca tcc atc aaa gct 277
59 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
60 20 25 30
62 ttg cgc aac gcc aac ctc agg cga gat gag agc aat cac ctc aca gac 325
63 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
64 35 40 45
66 ttg tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg 373
67 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
68 50 55 60
70 cag agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca 421

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71 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
72 65 70 75 80
74 tgg cgg ctt cac tct cag gag aat aca cgg ata cag cta gtg ttt gac 469
75 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
76 85 90 95
78 aat cag ttt gga tta gag gaa gca gaa aat gat atc tgt agg tat gat 517
79 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
80 100 105 110
82 ttt gtg gaa gtt gaa gat ata tcc gaa acc agt acc att att aga gga 565
83 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
84 115 120 125
86 cga tgg tgt gga cac aag gaa gtt cct cca agg ata aaa tca aga acg 613
87 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
88 130 135 140
90 aac caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa 661
91 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Tyr Phe Val Ala Lys
92 145 150 155 160
94 cct gga ttc aag att tat tat tct ttg ctg gaa gat ttc caa ccc gca 709
95 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
96 165 170 175
98 gca gct tca gag acc aac tgg gaa tct gtc aca agc tct att tca ggg 757
99 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
100 180 185 190
102 gta tcc tat aac tct cca tca gta acg gat ccc act ctg att gcg gat 805
103 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
104 195 200 205
106 gct ctg gac aaa aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc 853
107 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
108 210 215 220
110 aag tac ttc aat cca gag tca tgg caa gaa gat ctt gag aat atg tat 901
111 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
112 225 230 235 240
114 ctg gac acc cct cgg tat cga ggc agg tca tac cat gac cgg aag tca 949
115 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
116 245 250 255
118 aaa gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac agt tgc 997
119 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
120 260 265 270
122 act ccc agg aat tac tgc gtc aat ata aga gaa gag ctg aag ttg gcc 1045
123 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
124 275 280 285
126 aat gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga 1093
127 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
128 290 295 300
130 aat tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc aat tca 1141
131 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
132 305 310 315 320
134 ggg aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag cct ggc 1189
135 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly

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136          325          330          335
138 cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt gac atc 1237
139 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
140          340          345          350
142 cag ttg gat cac cat gaa cga tgt gat tgt atc tgc agc tca aga cca 1285
143 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
144          355          360          365
146 cct cga taagagaatg tgcacatcct tacattaagc ctgaaagaac ctttagttta 1341
147 Pro Arg
148          370
150 aggagggtga gataagagac ccttttccta ccagcaacca aacttactac tagcctgcaa 1401
152 tgcaatgaac acaagtgggt gctgagtctc agccttgctt tgtaaatgcc atggcaagta 1461
154 gaaaggtata tcatcaactt ctatacctaa gaatatagga ttgcatttaa taatagtgtt 1521
156 tgaggttata tatgcacaaa cacacacaga aatatattca tgtctatgtg tatatagatc 1581
158 aaatgttttt ttggtatat ataaccaggt acaccagagc ttacatatgt ttgagttaga 1641
160 ctcttaaaat cctttgccaa aataagggat ggtcaaatat atgaaacatg tctttagaaa 1701
162 atttaggaga taaatttttt tttaaatttt gaaacacaaa acaattttga atcttgctct 1761
164 cttaaagaaa gcatcttgta tattaaaaat caaaagatga ggctttctta catatacatc 1821
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178 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
179 20 25 30
181 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
182 35 40 45
184 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
185 50 55 60
187 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
188 65 70 75 80
190 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
191 85 90 95
193 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
194 100 105 110
196 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
197 115 120 125
199 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
200 130 135 140
202 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
203 145 150 155 160
205 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
206 165 170 175
208 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
209 180 185 190
211 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp

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212          195          200          205
214 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
215          210          215          220
217 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
218 225          230          235          240
220 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
221          245          250          255
223 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
224          260          265          270
226 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
227          275          280          285
229 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
230          290          295          300
232 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
233 305          310          315          320
235 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
236          325          330          335
238 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
239          340          345          350
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244 Pro Arg
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254 <221> NAME/KEY: CDS
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262 ttggattaga ggaagcagaa aatgatattc gtaggtatga ttttgtggaa gttgaagata 180
264 tatccgaaac cagtaccatt attagaggac gatggtgttg acacaaggaa gtctctccaa 240
266 ggataaaaac aagaacgaac caaattaaaa tcacattcaa gtccgatgac tactttgttg 300
268 ctaaacctgg attcaagatt tattattctt tgctggaaga ttccaaccc gcagcagctt 360
270 cagagaccaa ctgggaatct gtcacaagct ctatttcagg ggtatcctat aactctccat 420
272 cagtaacgga tcccaactctg attgcggatg ctctggacaa aaaaattgca gaatttgata 480
274 cagtggaaga tctgctcaag tacttcaatc cagagtcatt gcaagaagat cttgagaat 539
276 atg tat ctg gac acc cct cgg tat cga gcc agg tca tac cat gac cgg 587
277 Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg
278 1 5 10 15
280 aag tca aaa gtt gac ctg gat agg ctc aat gat gat gcc aag cgt tac 635
281 Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr
282 20 25 30
284 agt tgc act ccc agg aat tac tcg gtc aat ata aga gaa gag ctg aag 683
285 Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys
286 35 40 45

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288 ttg gcc aat gtg gtc ttc ttt cca cgt tgc ctc ctc gtg cag cgc tgt 731
289 Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys
290      50      55      60
292 gga gga aat tgt ggc tgt gga act gtc aac tgg agg tcc tgc aca tgc 779
293 Gly Gly Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys
294      65      70      75      80
296 aat tca ggg aaa acc gtg aaa aag tat cat gag gta tta cag ttt gag 827
297 Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu
298      85      90      95
300 cct ggc cac atc aag agg agg ggt aga gct aag acc atg gct cta gtt 875
301 Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val
302      100      105      110
304 gac atc cag ttg gat cac cat gaa cga tgt gat tgt atc tgc agc tca 923
305 Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser
306      115      120      125
308 aga cca cct cga taagagaatg tgcacatcct tacattaagc ctgaaagaac 975
309 Arg Pro Pro Arg
310      130
312 ctttagttta aggaggggtga gataagagac ctttttccta ccagcaacca aacttactac 1035
314 tagcctgcaa tgcaatgaac acaagtgggt gctgagtcct agccttgctt tgtaaagcc 1095
316 atggcaagta gaaagggtata tcatcaactt ctatacctaa gaatatagga ttgcatttaa 1155
318 taatagtgtt tgaggttata tatgcacaaa cacacacaga aatatattca tgtctatgtg 1215
320 tatatagatc aaatgttttt ttgtgtatat ataaccaggt acaccagagc ttacatatgt 1275
322 ttgagtttaga ctcttaaaat cctttgccaa aataagggat ggtcaaatat atgaaacatg 1335
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326 atcttgctct cttaaagaaa gcattcttga tattaaaaat caaaagatga ggctttctta 1455
328 catatacatc ttagttgatt attaaaaaag gaaaaatatg gtttccagag aaaaggccaa 1515
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347 Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys
348      35      40      45
350 Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys
351      50      55      60
353 Gly Gly Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys
354      65      70      75      80
356 Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu
357      85      90      95
359 Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val
360      100      105      110
362 Asp Ile Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser

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VERIFICATION SUMMARY

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Input Set : A:\Cura-77.app

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number